IN THE SPECIFICATION

[0017] FIGURE 1. Scatterplot showing detail view of sample data points $x_i \in R^n$ representing *H. pylori* ~~protein~~-protein-protein interactions, visualized by two dimensional Sammon mapping. Circled points indicate incorrect decisions made during leave-one-out prediction error estimation. 90% of all data points (1,873/2,077) ~~appearl~~ appear in this map. Coordinate axes contain arbitrary units. Estimated system generalization error rate is 12.04%.